IN THE CLAIMS

Please amend the claims as follows:

Claims 1-90 (Canceled)

Claim 91 (New): A method for analyzing data, comprising:

obtaining multiple sets of raw data from a primary source, wherein each data set has peaks having a defined position and area,

smoothing the peaks in each data set based on one or more user defined parameters using the ISEApeaks® software, and

storing each smoothed data set in a data file.

Claim 92 (New): The method of claim 91, further comprising assimilating the smoothed data from each data set into a peak database using ISEApeaks® software.

Claim 93 (New): The method of claim 91, wherein said raw data is obtained from a primary source selected from the group consisting of a growth culture, an electrophoretic sample, a chromatographic column, a blotting membrane, a centrifugation tube, and a microarray.

Claim 94 (New): The method of claim 91, wherein the multiple sets of raw data are obtained from an automated sequencer.

Claim 95 (New): The method of claim 91, wherein the multiple sets of raw data are obtained from a sequencer and contain peaks that correspond to a CDR3 (complementary determining region 3) hypervariable region from the beta chain of a T cell receptor.

Claim 96 (New): The method of claim 91, wherein the multiple sets of raw data are obtained from a high throughput analysis of data sets generally described by sets of peaks characterized by a position and an area.

Claim 97 (New): The method according to claim 96, wherein at least one bioinformatic tool which is a raw data extraction program or a DNA automatic sequencer is used to extract and smooth peak data sets according to parameter files and store them in data files.

Claim 98 (New): The method according to claim 96, wherein particular profiles representing peaks are created in a form suitable for analysis.

Claim 99 (New): The method according to claim 96, wherein a peak database is built.

Claim 100 (New): The method according to claim 99, wherein the peak database is analyzed by at least one statistical tool.

Claim 101 (New): The method according to claim 100, wherein analysis of the peak database is used to determine at least one prognostic or diagnostic criterion.

Claim 102 (New): The method according to claim 101, wherein the at least one prognostic and diagnostic criterion is used in the field of physiopathology.

Claim 103 (New): The method according to claim 102, wherein the at least one prognostic and diagnostic criterion is useful in the field of immunotherapy, cancer treatment, treatment of HIV, treatment of an infectious disease other than HIV, or treatment of an autoimmune disease.

Claim 104 (New): The method according to claim 96, wherein the data is obtained from the high throughput analysis of data sets representing an immune repertoire.

Claim 105 (New): The method according to claim 104, wherein said data is obtained by a process comprising:

purifying DNA or RNA fragments from cells defining an immune repertoire.

Claim 106 (New): The method according to claim 105, further comprising

synthesizing cDNA from purified RNA defining an immune repertoire,

amplifying the cDNA by a PCR or a SDA method using oligonucleotides specific for antigen specific receptor genes,

labeling the amplified DNA for detection by performing a runoff extension step with J or C specific oligonucleotide labeled with a fluorescent drug,

separating by electrophoresis each labeled amplified DNA on an automatic sequencer thus obtaining a set of electrophoregrams,

identifying peaks in said set of electrophoregrams by determining their position and area that correspond to labeled amplified DNA.

Claim 107 (New): The method according to claim 106, wherein said oligonucleotides specific for an antigen specific receptor gene are from the variable (V), junctional (J) and/or constant (C) regions of an immunoglobin receptor gene.

Claim 108 (New): The method according to claim 106, wherein said oligonucleotides specific for an antigen specific receptor gene are from the variable (V), junctional (J) and/or constant (C) regions of a T cell receptor gene.

Claim 109 (New): The method according to claim 106, further comprising reading the labeled amplified DNA.

Claim 110 (New): A method for analyzing data describing a T or B cell immune repertoire, comprising:

obtaining multiple sets of raw data from a DNA automatic sequencer or from a raw data extraction program, wherein each data set has peaks having a defined position and area,

smoothing the peaks in each data set based on one or more user defined parameters using the ISEApeaks® software, and

storing each smoothed data set in a data file.

Claim 111 (New): The method of claim 110, wherein said raw data describes CDR3 spectratypes.